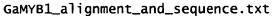
GamyB1_alignment_and_sequence.txt

Exhibit 2

gi 7438	345 p	oir T09879	myb-related protein A - upland cotton	
gi 4373	27 gb	AAA33067.1	MYB1 [Gossypium hirsutum]	
gi 2347	6277	gb AAN28269.1	myb-like transcription factor 1 [Gossypium hir	sutum]
Length = 294 Score = 602 bits (1553), Expect = e-171 Identities = 288/294 (97%), Positives = 291/294 (98%) Frame = +3				
Query:	144	MGRSPCCEKAHTNKGAWTK	EEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY 323 EEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY	
Sbjct:	1	MGRSPCCEKAHTNKGAWTK	EEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY 60	
Query:	324	LRPDLKRGNFTEEEDELII	KLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG 503	:
Sbjct:	61	LRPDLKRGNFTEEEDELII	KLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG KLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG 120	
Query:	504	IDPQTHRPLNQTAITNTVT	GPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL 683	
Sbjct:	121	IDPQTHRPLNQTA TNTVT IDPQTHRPLNQTANTNTVT	PTELDFRNSPTSVSKSSSIKNPSLDFNYNEF FKS+TDSL APTELDFRNSPTSVSKSSSIKNPSLDFNYNEFQFKSNTDSL 180	
Query:	684	EEPNCTASTGMTTDEEQQE	QLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK 863	
Sbjct:		EEPNCTAS+GMTTDEEQQE EEPNCTASSGMTTDEEQQE	QLHKKQQYGPSNGQDINLELSIGIVSADSSRVS+ANSAESK QLHKKQQYGPSNGQDINLELSIGIVSADSSRVSNANSAESK 240	
Query:		PKVDNNNFOFLEOAMVAKA	VCLCWOLGFGTSEICRNCONSNSNGFYSYCRPLDS 1025	
Sbjct:		PKVDNNNFOFLEOAMVAKA	VCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS VCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS 294	

>Contig20 GaMYB1 GGCACGAGACAGTTTCTCTTTTTTGCTCATTTCCATCATCCCCATGTCCC CTCTCCATGTTTTTCTAAATCTCTCCATATACCTATAACACCGTTATTCT TTCTCTATTCTACCTGATTTGATTTGATTTGATTTTGTAACTGATGGGAC GATCACCTTGTTGTGAAAAGGCTCATACCAACAAAGGTGCCTGGACCAAA GAGGAAGATCAACGCCTCATCAACTACATCCGTGTCCATGGTGAAGGCTG CTGGCGTTCCCTCCCCAAAGCTGCTGGGCTGCTTAGATGTGGTAAGAGTT GCAGATTAAGATGGATAAACTACTTGAGGCCTGATCTTAAGAGAGGAAAT TTCACTGAAGAAGAAGATGAGCTTATCATCAAGCTTCACAGTTTACTTGG AGATAAAGAACTACTGGAACACACACATCAAAAGAAAGCTTATAAGCAGA **GGAATTGATCCACAAACTCATCGTCCTCTCAATCAAACGGCCATTACCAA** CACAGTCACAGGCCCCACCGAATTGGATTTCAGAAACTCGCCCACATCCG TTTCCAAATCCAGTTCCATCAAAAACCCGTCTCTGGATTTCAATTACAAT GAATTTCATTTCAAGTCCCACACAGATTCCCTTGAAGAACCCAACTGTAC AGCCAGCACTGGCATGACTACAGATGAAGAACAACAAGAACAGCTGCACA AGAAGCAGCAATACGGTCCGAGCAATGGGCAAGACATAAATTTGGAGCTG TCGATTGGGATTGTTTCAGCTGACTCATCTCGGGTATCAAGTGCCAACTC GGCCGAGTCGAAACCAAAGGTAGATAACAACAATTTCCAGTTTCTTGAAC AAGCTATGGTGGCTAAGGCGGTATGTTTGTGTTTGGCAATTAGGTTTTGGA ACAAGTGAAATTTGTAGGAACTGTCAAAATTCAAATTCAAATGGCTTCTA TAGTTATTGTAGACCCTTGGATTCATAGGGTCATCTTTTTCTTCTT CACTGTAATCAAAGCAAAATTATAAAACAAAGACTCTTTTTGATTTGTTC AATTTATAGGTTCAAAAAAAAAAAAAAAAAA



>Contig20_Frame+3 GamyB1
HETVSLFCSFPSSPCPLSMFF*ISPYTYNTVILSLFYLI*FDLIL*LMGRSPCCEKAHTN
KGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEE
EDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRGIDPQTHRPLNQTA
ITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSLEEPNCTASTGMTT
DEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESKPKVDNNNFQFLEQ
AMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS*GHLFLLSFCF*EIN*FLI
IIFLPAHCNQSKIIKQRLFLICSIYRFKKKKKK

>GAMYB1 - putative from GhMYB1 alignment
MGRSPCCEKAHTNKGAWTKEEDQRLINYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY
LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG
IDPQTHRPLNQTAITNTVTGPTELDFRNSPTSVSKSSSIKNPSLDFNYNEFHFKSHTDSL
EEPNCTASTGMTTDEEQQEQLHKKQQYGPSNGQDINLELSIGIVSADSSRVSSANSAESK
PKVDNNNFQFLEQAMVAKAVCLCWQLGFGTSEICRNCQNSNSNGFYSYCRPLDS